Amendments to the Specification:

Please amend the specification before its first line by inserting as a separate paragraph:

This is a continuation of U.S. application no. 09/700,187 filed November 13, 2000, now abandoned.

In the Brief Description of the Drawings of the specification, please amend the paragraph at page 6, lines 18 – 27 as follows:

FIG. 1 shows the nucleotide sequence and the amino acid sequence of the pra2 genomic gene referring to the nucleotide sequence number on the right with the transcription start point being 0 (indicated by ↓) and the amino acid sequence number on the left. The arrow heads indicate the exon-intron boundary and the 113-bp inverted homologous sequence is underlined with the inverted repeat sequence being indicated by opposite arrows. The 93-bp cis-element and the TATA box are boxed and the 12-bp core sequence is shaded. The nucleic sequence is SEQ ID NO: 41 and the amino acid sequence is SEQ ID NO: 42.

In the Brief Description of the Drawings of the specification, please amend the paragraph at page 8, line 23 to page 9, line5 as follows:

FIG. 6 shows the results of linker scanning analysis of the core sequence. Panel a) shows the nucleotide sequences of the wild type and mutants near the core sequence in the structure of PL4A shown in Fig. 5, with base changes from the wild type being lowercased. Panel b) shows expression levels of the reporter gene 12

hours after bombardment of deletion clones having the structures shown in panel a) into etiolated stems of pea, in which D represents a dark condition and R represents a dark condition for 12 hours after red light irradiation for 2 minutes. WT is SEQ ID NO: 29, LS1 is SEQ ID NO: 43, LS2 is SEQ ID NO: 44, LS3 is SEQ ID NO: 45, LS4 is SEQ ID NO: 46 and LS5 is SEQ ID NO: 47.

In the Brief Description of the Drawings of the specification, please amend the paragraph at page 9, lines 6 – 14 as follows:

FIG. 7 shows the results of a gel shift assay. Panel a) shows the sequences of synthetic DNAs used in the experiment, in which WT and MT represent the sequences of the wild-type and a mutant, respectively. Panel b) shows the results of the gel shift assay, in which D and L represent extracts prepared from pea epicotyls grown in the dark or illuminated for 6 hours, respectively. The arrow indicates the electrophoretic position of synthetic DNA-protein complexes. WT (upper) is SEQ ID NO: 29, WT (lower) is SEQ ID NO: 30, MT (upper) is SEQ ID NO: 31 and MT WT (lower) is SEQ ID NO: 32.